

Genome Wide Association Study of Substance Use Disorder in the United Arab Emirates population

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Background: Substance Use Disorder (SUD) is a global problem with no boundaries, which also afflicts individuals from countries of the Arabian Peninsula. In an effort to develop targeted prevention and intervention initiatives in the United Arab Emirates (UAE), this study was conceived to identify genetic factors contributing to the SUD in a first-ever cohort that was systematically recruited from the country's National Rehabilitation Centre (NRC) in Abu Dhabi. It is also, the first Genome Wide Association Study (GWAS) for SUD conducted in the Middle East.

Methods: Two hundred and fifty male patients were recruited from the NRC. Information on substance use was collected using a questionnaire that was completed at an interview with patients who consented to participate. Two hundred and sixty-two male subjects from the Emirates Family Registry (EFR) were used as a comparison group. SNP genotyping for rs1076560 and rs1799971 was performed using TaqMan® SNP genotyping assay on viiA™7 (Applied Biosystems Inc. (ABI); Foster City, CA, USA). The GWAS was conducted using Illumina Omni Exome5 microarray technology. Various statistical tools were used to analyse the data including: Plink (Broad Institute, MIT and Harvard), R (The R package for statistical computing) and *i-GSEA4GWAS* web server (Zhang.*et al*, 2010).

Results: There were no significant associations observed for *DRD2* SNP rs1076560, *OPRM1* SNP rs1799971 and combined genotypes of both SNPs in the SUD group. From the GWAS three rare genetic variants identified indicating association with SUD. The results replicated in an Australian case_control cohort for validation.

Conclusion: This study highlights the importance of examining the refined criteria of phenotypes. Pathway analysis of the identified variants need to be investigated in the development or progression of the disorder. Underpinning the genetic factors will contribute to establish specific prevention and intervention strategies, targeting differences between these distinct genetic profiles will capture a large subset of sufferers. Future genetic studies have to expand in order to include possible epigenetic relationships.